

Appln No.: 10/078,650 Page 1 Applicant(s): Katsumi Fujimoto et al.
NOVEL BHLH TYPE TRANSCRIPTION FACTOR GENES
DEC2

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hDEC2a DEC1

MDEGIPHLQERQLLEHRDFIGLDYSSLYMC-KPKRSMKRD-DTKDTYKLPHRLIEKKRRDRIN M-ERIPSAQPPPACLPKAPGLEHGDLPGMYPAHMYQVYKSRRGIKRSEDSKETYKLPHRLIEKKRRDRIN	
ECIAQLKOLLPEHLKLTTLGHLEKAVVLELTLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSD ECIAQLKOLLPEHLKLTTLGHLEKAVVLELTLKHVKALTNLIDQQQQKIIALQSGLQAGELSGR-NVETG	
LDAFHSGFQTCAKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPS QEMFCSGFQTCAREVLQYLAKHEN-T-RDLKSSQLVTHLHRVVSELLQGGTSRKPSDPAPKVMDFKEKPS	
A-A-GSAAAPCLERAGQKLEPLAYCVPVIQRTQP-SAELAAENDTDTDSGYGGEAEARPD-R-EK- SPAKGSEG-PG-KNCVPVIQRTFAHSSGEQSGSDTDTDSGYGGESEKG-DLRSEQPCFKS	
GKGAGASRVTIKQEPPGEDSPAPK-RMKL-DSRGGG-SGGGPGGGAAAAAALLGPDPAAAAALLR DHGRRFTMGERIGAIKQESE-E-PPTKKNRMQLSDDEGHFTSS	
PDAALLSSLVAFGGGGGAPFP-QPAAAAAPFCLPFCFLSP-SAAAAYVQPFLDKSGLEKYLYPAAAAAPFLISSPFLGPFCLPF-YLIPPSATA-YL-PMLEKCWYPTSVP-	
PLLYPGIPAPAAAAAAAAAAAAAAAFPCLSSVLSPPPEKAGAAAATLL-PHEVAPLGAPHPQHPHGRTH VL-YPGLNASAAALSSFMNP-DKISAPLLMPQRLPSP	
LPFAGPREPGNPESSAQE-DPSQPGK-EA-P LP-AHPSVDSSVLLQALKPIPPLNLETKD	4.82
(Homo Logy 43%)	

(Hollio logy 45%)

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DEC<sub>2</sub>

hDEC2a hDEC2b

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTK--DTYKLPHRLIEKKRRDRINECIAQLK 68 MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTKVSDTYKLPHRLIEKKRRDRINECIAQLK 70

DLLPEHLKLTTLGHLEKAVVLELTLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLDAFHSGFQTC 138 DLLPEHLKLTTLGHLEKAVVLELTLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLDAFHSGFQTC 140

AKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSAAAPCLERAG 208 AKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSAAAPCLERAG 210

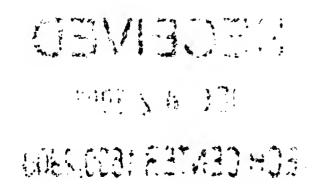
QKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGEAEARPDREKGKGAGASRVTIKQEPPGEDSPAPK 278 QKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGEAEARPDREKGKGAGASRVTIKQEPPGEDSPAPK 280

RMKLDSRGGGGGGGGGAAAAAAALLGPDPAAAAALLRPDAALLSSLVAFGGGGGAPFPQPAAAAAPFC 348 RMKLDSRGGGGGGGGGAAAAAAALLGPDPAAAAALLRPDAALLSSLVAFGGGGGAPFPQPAAAAAPFC 350

LPFCFLSPSAAAAYVQPFLDKSGLEKYLYPAAAAAPFPLLYPGIPAPAAAAAAAAAAAAAAAAFPCLSSV 418 LPFCFLSPSAAAAYVQPFLDKSGLEKYLYPAAAAAPFPLLYPGIPAPAAAAAAAAAAAAAAAAFPCLSSV 420

LSPPPEKAGAAAATLLPHEVAPLGAPHPQHPHGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP 482 484 LSPPPEKAGAAAATLLPHEVAPLGAPHPQHPHGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP

FIG. 2



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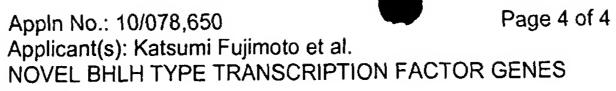
DEC2

hDEC2a mDEC2a

DEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTKDTYKLPHRLIEKKRRDRINECIAQLKDI	- 70
IDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSLKRDDTKDTYKLPHRLIEKKRRDRINECIAQLKDI	. 70
PEHLKLTTLGHLEKAVVLELTLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLDAFHSGFQTCAF	( 14(
PEHLKLTTLGHLEKAVVLELTLKHLKALTALTEQQHQKIIALQNGERSLKSPVQADLDAFHSGFQTCAK	( 140
VLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSK-GTG-AP-SAAGSAAAPCLERA	207
VLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQVP-SGRGSGRAPCSA-G-AAAA	196
-GQKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGEAEARPDREKGKGAGASRVTIKQEPPGEDS-P	275
GPERVARCVPVIQRTQPGTEP-EHDTDTDSGYGGEAE-QG-RA-AVKQEPPG-DSSP	249
PKRMKLDSRGGGGGGGGGAAAAAALLGPDPAAAAALLRPDAALLSSLVAFGGGGGAPFPQPAAAAA	345
PKRPKLEARGGGGAPFAQPAAALLGSLVALGGGAPFAQPAAA	288
FCLPFCFLSPSAAAAYVQPFLDKSGLEKYLYPAAAAAAPFPLLYPGIPAPAAAAAAAAAAAAAAAAFPCL	415
FCLPFYLLSPSAAA-YVQPWLDKSGLDKYLYPAAAA-PFPLLYPGIPAAAAAAAAAAAAFPCL	348
SVLSPPPEKAGA-AAATLLPHEVAPLGAP-HPQHPHGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP	482
SVLSPPPEKAGATAGAPFLAHEVAPPG-PLRPQHAHSRTHLPRAVNPESS-QEDATQPAKDAP	410

FIG. 3

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DEC2

h0EC2a mDEC2a

SHARP-1

	MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTKDTYKLPHRLIEKKRRDRINECIAQLKDL	70
•	MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSLKRDDTKDTYKLPHRLIEKKRRDRINECIAQLKDL	70
	MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSLKRDDTKDTYKLPHRLIEKKRRDRINECIAQLKDL	70
~		
	LPEHLKLTTLGHLEKAVVLELTLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLDAFHSGFQTCAK	140
	LPEHLKLTTLGHLEKAVVLELTLKHLKALTALTEQQHQKIIALQNGERSLKSPVQADLDAFHSGFQTCAK	140
	LPEHLKLTTLGHLEKAVVLELTLKHLKALTALTEQQHQKIIALQNGERSLKSPVQADLDAFHSGFQTCAK	140
	EVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSK-GTG-AP-SAAGSAAAPCLERA	207
	EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQVP-SGRGSGRAPCSA-G-AAAA	
	EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQVT-PGRGPGRAPCSA-G-AAAA	סצו
	-GQKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGEAEARPDREKGKGAGASRVTIKQEPPGEDS-P	275
	SGP-ERVARCVPVIQRTQPGTEP-EHDTDTDSGYGGEAE-QG-RA-A-VKQEPPG-DSSP	249
•	SGS-ERVARCVPVIQRTQPGTEP-EHDTDTDSGYGGEAE-QG-RA-A-VKQEPPG-DPSL	249
	ADVDMVI DODGGGGGGGGGAAAAAAI I GDDDAAAAAI I DDDAAI I OO WAEGGGGGADEDODAAAAA	245
	APKRMKLDSRGGGGGGGGAAAAAALLGPDPAAAAALLRPDAALLSSLVAFGGGGGAPFPQPAAAAA	
	APKRPKLEARGALLGPEPALLGSLVALGGGAPFAQPAAA-	
<i>J</i> .	RPRG .	253
•	PFCLPFCFLSPSAAAAYVQPFLDKSGLEKYLYPAAAAAPFPLLYPGIPAPAAAAAAAAAAAAAAAAFPCL	415
	PFCLPFYLLSPSAAA-YVQPWLDKSGLDKYLYPAAAA-PFPLLYPGIPAAAAAAAAAAFPCL	348
	SSVLSPPPEKAGA-AAATLLPHEVAPLGAP-HPQHPHGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP	482
	SSVLSPPPEKAGATAGAPFLAHEVAPPG-PLRPQHAHSRTHLPRAVNPESS-QEDATQPAKDAP	410